

AMENDMENT

In the claims:

Claim 1 (Original): A method for determining a human's capacity to metabolize a substrate of a CYP2D6 enzyme, said method comprising the steps of:

a) isolating single stranded nucleic acids from the human, said nucleic acids encoding 5' flanking regions of CYP2D6 genes present on each homologous chromosome 22 of the human, wherein said region is represented by a sequence as set forth in SEQ ID NO:2; and

b) detecting at least three polymorphisms within the region, wherein the polymorphisms are selected from the group consisting of nucleotides present at polymorphic sites represented by positions 36, 194, and 942 of SEQ ID NO:2; nucleotides present at polymorphic sites represented by positions 36, 620, and 942 of SEQ ID NO:2; nucleotides present at polymorphic sites represented by positions 36, 194, and 880 of SEQ ID NO:2; nucleotides at polymorphic sites represented by positions 36, 620, and 880 of SEQ ID NO:2; nucleotides at polymorphic sites represented by positions 36, 194, 620, and 880 of SEQ ID NO:2; nucleotides at polymorphic sites represented by positions 36, 194, 620, and 942 of SEQ ID NO:2; nucleotides at polymorphic sites represented by positions 36, 620, 880, and 942 of SEQ ID NO:2; and nucleotides at polymorphic sites represented by positions 36, 194, 620, 880, and 942 of SEQ ID NO:2.

Claims 2-8 (Canceled)

Claim 9 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 194, and 942 of SEQ ID NO:2 are detected.

Claim 10 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 620 and 942 of SEQ ID NO:2 are detected.

Claim 11 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 194 and 880 of SEQ ID NO:2 are detected.

Claim 12 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 620 and 880 of SEQ ID NO:2 are detected.

Claim 13 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 194, 620 and 880 of SEQ ID NO:2 are detected.

Claim 14 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 194, 620 and 942 of SEQ ID NO:2 are detected.

Claim 15 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 620, 880 and 942 of SEQ ID NO:2 are detected.

Claim 16 (Previously presented): The method of claim 1, wherein nucleotides at the polymorphic sites represented by positions 36, 194, 620, 880 and 942 of SEQ ID NO:2 are detected.